

## Prix D.Day – SVSN



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Prix du meilleur poster ou présentation orale  
de la journée des doctorants  
de la Faculté de Biologie et Médecine 2011

## Genetic structure of *cannabis sativa*: from population genomics to forensic applications

*par*

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Hemp (*Cannabis sativa*) was domesticated over 7,000 years ago as a source of fibre, food, and medicines. Besides its agroeconomical importance, *C. sativa* is also used as a recreational drug (i.e. marijuana or hashish), due to the presence of tetrahydrocannabinol (THC), a cannabinoid compound with psychoactive properties. Morphology and cannabinoid content vary extensively between populations and individuals. As a result, the differentiation between licensed fibre and prohibited drug varieties of *C. sativa* poses a major impediment to the development of the industrial and therapeutic potential of this controversial species.

Hence, in this study we want to understand the genetic effects of human domestication and selection on patterns of genetic diversity within and among populations. Moreover, we analyze the potential for creating an effective forensic tool to distinguish between drug and agricultural varieties based on genetic differentiation. Therefore, we genotyped 24 agricultural *Cannabis* populations (839 individuals) and 25 drug varieties (507 individuals) for 13 microsatellite loci. Clustering analyzes revealed the presence of two distinct genetic clusters separating drug and crop varieties. Further assignment tests of 120 known *Cannabis* samples showed that each of them has been correctly assigned to either the drug or fibre cluster. Genetic diversity analyzes also demonstrated that allelic richness was significantly lower for drug (2.19  $p < 0.001$ ) than for crop varieties (3.44  $p < 0.001$ ). In addition, we found higher genetic differentiation among drug populations ( $F_{st}$ : 0.424  $p < 0.001$ ) than among agricultural populations ( $F_{st}$ : 0.147  $p < 0.001$ ). This might be due to an intense selection for specific phenotypes (bottleneck) and the use of clonal reproduction (especially for drugs).

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## Molecular basis and regulation of insecticidal activity in plant root-associated pseudomonads

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Fungal diseases and insect pests cause major damage to agricultural crops and they are very difficult to control, in particular when below-ground plant parts are affected. *Pseudomonas fluorescens* are well-known disease suppressive bacteria in the rhizosphere of various plant species. The plant-beneficial *P. fluorescens* strain CHA0 produces many secondary metabolites which protect the plant roots against fungi and was recently discovered to also exhibit potent systemic and oral insecticidal activity.

The anti-insect action of CHA0 depends on the production of a novel large protein toxin termed Fit, for *P. fluorescens* insecticidal toxin, and additional yet unidentified bacterial factors. While non-toxic *Escherichia coli* can be rendered lethal to insects by transgenic expression of the toxin gene, Fit toxin-negative mutants of *P. fluorescens* are less virulent to insect larvae. The Fit toxin is part of a virulence cassette coding for regulators and a type I protein secretion system predicted to function in toxin export.

We try to identify mechanisms and signals that control the production, secretion and biological activity of the novel toxin and accessory virulence factors, and to understand their ecological role in the plant root environment. To answer our major research questions we make use of fluorescent proteins, toxin-specific antibodies, epifluorescence and electron microscopy, qRT-PCR, various insect and microanimal models, plant assays, and further techniques of molecular biology.

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